1

SEQUENCE LISTING

<110> KOBAYASHI, KAZUO
       KITAGAWA, YOSHINORI
       KOMEDA, TOSHIHIRO
       KAWASHIMA, NAGAKO
       JIGAMI, YOSHIFUMI
       CHIBA, YASUNORI

<120> METHYLOTROPH PRODUCING MAMMALIAN TYPE SUGAR CHAIN

<130> 081356-0224

<140> 10/511,436
<141> 2004-10-25

<150> PCT/JP03/05464
<151> 2003-04-28

<150> JP 2002-127677
<151> 2002-04-26

<160> 121

<170> PatentIn Ver. 3.3

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      Ogataea minuta GAP gene

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<213> Ogataea minuta

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<212> PRT
<213> Ogataea minuta

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Val Leu Arg Ile Ala Leu Ser Arg Lys Asp Ile Asn Val Val Ala Val
            20   25   30

Asn Asp Pro Phe Ile Ala Ala Glu Tyr Ala Ala Tyr Met Phe Lys Tyr
         35   40   45

Asp Ser Thr His Gly Arg Tyr Gln Gly Glu Val Thr Phe Glu Gly Lys
     50   55   60

Tyr Leu Val Ile Asp Gly Gln Lys Ile Glu Val Phe Gln Glu Arg Asp
 65   70   75   80

Pro Ala Asp Ile Pro Trp Gly Lys Glu Gly Val Asp Phe Val Ile Asp
             85   90   95

Ser Thr Gly Val Phe Thr Thr Thr Ala Gly Ala Gln Lys His Ile Asp
            100   105   110

Ala Gly Ala Lys Lys Val Ile Ile Thr Ala Pro Ser Ala Asp Ala Pro
         115   120   125

Met Phe Val Met Gly Val Asn His Lys Glu Tyr Thr Lys Asp Leu Ser
     130   135   140

Ile Val Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala
145   150   155   160

Lys Val Val Asn Asp Val Phe Gly Ile Glu Ser Gly Leu Met Thr Thr
                165   170   175

Val His Ser Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser His
            180   185   190

Lys Asp Trp Arg Gly Gly Arg Thr Ala Ser Gly Asn Ile Ile Pro Ser
         195   200   205

Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Leu Pro Ala Leu Ala
     210   215   220

Gly Lys Leu Thr Gly Met Ser Leu Arg Val Pro Thr Thr Asp Val Ser
225   230   235   240

Val Val Asp Leu Thr Val Asn Leu Lys Thr Pro Thr Thr Tyr Ala Glu
                245   250   255

Ile Ser Ala Ala Ile Lys Lys Ala Ser Glu Gly Glu Leu Ala Gly Ile
        260   265   270

Leu Gly Tyr Thr Glu Asp Ala Val Val Ser Thr Asp Phe Leu Thr Asp
        275   280   285

Asn Arg Ser Ser Ile Phe Asp Ala Ser Ala Gly Ile Leu Leu Thr Pro
   290   295   300

Thr Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Tyr Gly Tyr Ser
305   310   315   320

Thr Arg Val Val Asp Leu Leu Glu His Val Ala Lys Val Ser Ser Ala
        325   330   335

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<211> 1491
<212> DNA
<213> Ogataea minuta

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gtccactttt ctccaatagt atttgacccg ggttgctctc tgttgatttt ttctagatca 1440
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<210> 8
<211> 524
<212> DNA
<213> Ogataea minuta

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ttattttttta catctctgca ccggaaaact ggctatttga aaaatttcga cgttttgctt 180

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gaaactcgag ttgaggagca ttgccaaatt cgatcgtttt ctaacggacg ccagtcgagt 240
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atgtgctctt ctgctttttt ggtgaccaaa cgagatgaca attgactgca ttgaaaaggt 480
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<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer for production of an expression cassette
      with GAP gene promoter and terminator from
      Ogataea minuta

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<210> 10
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<212> DNA
<213> Artificial Sequence

<220>
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      primer for production of an expression cassette
      with GAP gene promoter and terminator from
      Ogataea minuta

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<210> 11
<211> 12
<212> PRT
<213> Saccharomyces cerevisiae

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<210> 12
<211> 11
<212> PRT
<213> Saccharomyces cerevisiae

<400> 12
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  1               5                  10
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<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
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      Ogataea Minuta URA3 gene

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<223> a, c, g or t

<220>
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<220>
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<223> a, c, g or t

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<210> 14
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
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      Ogataea Minuta URA3 gene

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<211> 3113
<212> DNA
<213> Ogataea minuta

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gaggttccta ccgcggacgg gtccaaagtg gaggttctcc gaaacatgtc tgtcgagacg 180
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Met Ser Ser Thr Lys Thr Tyr Ala Gln Arg Ala Ala Ala His Pro Ser
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Pro Val Ala Arg Arg Leu Leu Asn Leu Met Glu Ser Lys Lys Thr Asn
            20                  25                  30

Leu Cys Ala Ser Val Asp Leu Thr Ser Thr Lys Asp Leu Leu Glu Leu
        35                  40                  45

Leu Asp Lys Leu Gly Pro Phe Ile Cys Leu Val Lys Thr His Ile Asp
    50                  55                  60

Ile Val Glu Asp Phe Ser Tyr Glu Asn Thr Val Val Pro Leu Leu Lys
65                  70                  75                  80
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Leu Ala Lys Lys His Asn Phe Met Ile Phe Glu Asp Arg Lys Phe Ala
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            100   105   110

Ile Ala Lys Trp Ala Asp Ile Thr Asn Ala His Gly Val Thr Gly Ser
            115   120   125

Arg Ile Val Ser Gly Leu Arg Gln Ala Ala Gln Glu Thr Thr Asp Glu
        130   135   140

Pro Arg Gly Leu Leu Met Leu Ala Glu Leu Ser Ser Glu Gly Ser Leu
145   150   155   160

Ala Tyr Gly Glu Tyr Thr Lys Lys Thr Val Glu Ile Ala Lys Ser Asp
                165   170   175

Arg Asp Phe Val Ile Gly Phe Ile Ala Gln Asn Asp Met Gly Gly Arg
            180   185   190

Asp Glu Gly Phe Asp Trp Leu Ile Met Thr Pro Gly Val Gly Leu Asp
            195   200   205

Asp Thr Gly Asp Ala Leu Gly Gln Gln Tyr Arg Thr Val Ser Ala Val
        210   215   220

Met Lys Thr Gly Thr Asp Ile Ile Ile Val Gly Arg Gly Leu Phe Gly
225   230   235   240

Lys Gly Arg Asp Pro Val Val Glu Gly Glu Arg Tyr Arg Lys Ala Gly
                245   250   255

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<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer for amplification of a gene fragment
      conferring resistance against chloramphenicol

<400> 17
atggagaaaa aaactagtgg atataccacc   30

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

```
<220>
<223> Description of Artificial Sequence: Synthetic
      primer for amplification of a gene fragment
      conferring resistance against chloramphenicol

<400> 18
ctgagacgaa aaagatatct caataaaccc                                    30


<210> 19
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DU5 used for confirmation of destruction
      of Ogataea minuta URA3 gene

<400> 19
aggaagaaga ggaggaagag gaagaaac                                      28


<210> 20
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DUC5 used for confirmation of destruction
      of Ogataea minuta URA3 gene

<400> 20
cgatgccatt gggatatatc aacggtgg                                      28


<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DU3 used for confirmation of destruction
      of Ogataea minuta URA3 gene

<400> 21
ccgtgtttga gtttgtgaaa aaccagggc                                     29


<210> 22
<211> 28
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DUC3 used for confirmation of destruction
      of Ogataea minuta URA3 gene

<400> 22
tgtggcgtgt tacggtgaaa acctggcc   28

<210> 23
<211> 14
<212> PRT
<213> Saccharomyces cerevisiae

<400> 23
Phe Val Ala Thr Asp Arg Ile Ser Ala Tyr Asp Val Ile Met
  1   5   10

<210> 24
<211> 14
<212> PRT
<213> Saccharomyces cerevisiae

<400> 24
Gln Asp Ser Tyr Asp Lys Gln Phe Leu Arg Asp Trp Leu Thr
  1   5   10

<210> 25
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PAD5 for amplification of 5'-region of
      Ogataea minuta ADE1 gene

<220>
<221> modified_base
<222> (6)
<223> a, c, g or t

<220>
<221> modified_base
<222> (9)
<223> a, c, g or t

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (18)
<223> a, c, g or t

```
<220>
<221> modified_base
<222> (24)
<223> a, c, g or t

<220>
<221> modified_base
<222> (27)
<223> a, c, g or t

<220>
<221> modified_base
<222> (36)
<223> a, c, g or t

<400> 25
ttygtngcna cngaymgnat hwsngcntay gaygtnatha tg                    42


<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PAD3 for amplification of 3'-region of
      Ogataea minuta ADE1 gene

<220>
<221> modified_base
<222> (3)
<223> a, c, g or t

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (15)
<223> a, c, g or t

<220>
<221> modified_base
<222> (33)
<223> a, c, g or t

<400> 26
gtnarccart cncknarraa ytgyttrtcr tanswrtcyt g                     41


<210> 27
<211> 2560
<212> DNA
<213> Ogataea minuta
```

<400> 27
```
gatatcccaa gaacctatgc cgagggttca gctcacggcc gataaaccaa tcaaagacaa 60
cgtttcctga gtttcctcca acggccagga ttatctcgtg agttcccaga ccgttcggct 120
tgcgtgtggg cacgaacgag cccacgtaga caaacaggct caaagccaac gaaaactcgt 180
acgcagtcac catcaattcc agaaagttct cgtggatgaa cgacagctca ggaaggttga 240
actttgtgag ataagctctg ctggcaagaa ttcccacgag aagagtgctc aattctttcc 300
cgttgacgag atagttgagc tttgttccgt ctcgtaacag gactccctct ttatggtagc 360
caggcatcac aagatccacc aacgtcagag tgaagaacca caccaggtaa accttccagc 420
acgtgacatt taacacaaga tcccgccagt tgccgactat cttggactcg aaaagcgttt 480
tcagcgtggc aaaatcgatg cttgcgcctt caaccacata ctcctcatta cagcaaaagt 540
agaggaaaag gaccactgaa gggagaaata ctgacaaaac gaccgctccc ggtgtcccgc 600
agaaatcttt atgcgtagtc ttggggttca attcagacat ggtagattgg tgagggtaat 660
tgtgaagagg attcgataaa gagaggggaa cagcaccgga gatagttctt agatcaaaat 720
gtttttctga ccttttttgc tctttctcgt ttagctcgcg tacagtcgac gcgtcggttt 780
gcgtcgaaaa gagtcaagcc gcgatcgcga ttaaaaatga atccggagaa gtcaaaaata 840
tgtaatttaa accatcacag tatataagta ggcgggaagc gcacaatttc taggcattcc 900
acagatcagc taaccaggac attccactgg agccaacaat gtcactcaca acaaccaacc 960
tcgacggcat cttgccgcta attgccaagg gcaaagtcag agacatctat caagttgacg 1020
aggaaagcct gctgttcgtg gcaacagacc ggattccgc ctacgatgtg atcatggaga 1080
atggaatcaa agacaagggt aaaatactga ctcagctgtc agtattctgg tttgatttgc 1140
tgaaagacac tatcaagaac caccttatcg catccactga cgacgaagtg tttgccagac 1200
ttccacagga gctgtctcag ccaaagtaca agtcgcagct gagtggaaga gcactggtgg 1260
tgagaaagca caaattgatc cccctggagg tgattgtcag aggctacatc accggaagtg 1320
catggaagga gtacaacaag agcaagaccg tgcacggtct cgaggttggc gcagagctga 1380
aggagagtca agagttcccc gttccgattt tcaccccgtc aacgaaagct gaacaaggcg 1440
aacacgacga aaacatttcc cccgagaaag ctgcagagat tgtcggggaa caactgtgtg 1500
cgcggctcgc agaaaaggct gtgcagctgt actccaaggc cagaacttac gccaaaagca 1560
agggtatcat tctcgccgac acaaagtttg agtttggaat tgacgagaac gacgaattgg 1620
ttcttgtgga cgaggttttg acccctgatt cctcgagatt ttgggacgca aagacttaca 1680
agatcggaca gtcgcaggac tcttacgaca aacagtttct gagagactgg ctcacgtcca 1740
acggtctgaa cgggaaagac ggtgtctcta tgaccgcgga gatcgctgaa cgcacgggtg 1800
cgaagtacgt cgaggcattt gagtctctga cgggaagaaa gtggacgtag tttttgataa 1860
tagtaaccct ggaaatttga tatgtggcgg tgtagtctgt ggcggtggaa taaaatctaa 1920
attgaattta gtcgcttccc aaaacagcaa tttgtcaaca cttagtctgt gcacagcctt 1980
gacggcattt gagccatccc agggtctggc agttacaggg ctttgatcaa aagaaaactg 2040
gtgaagtttg acaacaggct acagctgcca agtcgcaact tgggtagtag ctcattcgtc 2100
gaacaccagt gcgccatgtc catcgccaac gagttccagc ccttggagct tattggtagg 2160
ggttcctttg gatgtgttcg gaaagtgcgc cgcaagtcgg acggcaagat atttgtgaga 2220
aaggagatct cctacatcgc catgaacacc aaagagaagc agcagctcac agcagagttt 2280
cgtattctca gagaactaaa gcatcccaac attgtccatt atgtccacca cgaccacgtc 2340
caggaggaac agaccgtcca tctgtacatg gaatactgcg atggggggcga cttgtcggtg 2400
ttgatcagga agtacaaagg aaagaacgag tttatcccgg agaacttgat ctggcaaatc 2460
ttcacccagg ttctcaacgc tctctatcaa tgccactatg gggtcaatat tgaggctgtg 2520
caagaacttt tccagtccac tccagagatt gcaccccggg 2560
```

<210> 28
<211> 303
<212> PRT
<213> Ogataea minuta

<400> 28
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Met Ser Leu Thr Thr Thr Asn Leu Asp Gly Ile Leu Pro Leu Ile Ala
 1               5                   10                  15


Lys Gly Lys Val Arg Asp Ile Tyr Gln Val Asp Glu Glu Ser Leu Leu
             20                  25                  30
```

Phe Val Ala Thr Asp Arg Ile Ser Ala Tyr Asp Val Ile Met Glu Asn
        35   40   45

Gly Ile Lys Asp Lys Gly Lys Ile Leu Thr Gln Leu Ser Val Phe Trp
    50   55   60

Phe Asp Leu Leu Lys Asp Thr Ile Lys Asn His Leu Ile Ala Ser Thr
65   70   75   80

Asp Asp Glu Val Phe Ala Arg Leu Pro Gln Glu Leu Ser Gln Pro Lys
            85   .   90   95

Tyr Lys Ser Gln Leu Ser Gly Arg Ala Leu Val Val Arg Lys His Lys
        100   105   110

Leu Ile Pro Leu Glu Val Ile Val Arg Gly Tyr Ile Thr Gly Ser Ala
        115   120   125

Trp Lys Glu Tyr Asn Lys Ser Lys Thr Val His Gly Leu Glu Val Gly
    130   135   140

Ala Glu Leu Lys Glu Ser Gln Glu Phe Pro Val Pro Ile Phe Thr Pro
145   150   155   160

Ser Thr Lys Ala Glu Gln Gly Glu His Asp Glu Asn Ile Ser Pro Glu
            165   170   175

Lys Ala Ala Glu Ile Val Gly Glu Gln Leu Cys Ala Arg Leu Ala Glu
            180   185   190

Lys Ala Val Gln Leu Tyr Ser Lys Ala Arg Thr Tyr Ala Lys Ser Lys
        195   200   205

Gly Ile Ile Leu Ala Asp Thr Lys Phe Glu Phe Gly Ile Asp Glu Asn
    210   215   220

Asp Glu Leu Val Leu Val Asp Glu Val Leu Thr Pro Asp Ser Ser Arg
225   230   235   240

Phe Trp Asp Ala Lys Thr Tyr Lys Ile Gly Gln Ser Gln Asp Ser Tyr
            245   250   255

Asp Lys Gln Phe Leu Arg Asp Trp Leu Thr Ser Asn Gly Leu Asn Gly
        260   265   270

Lys Asp Gly Val Ser Met Thr Ala Glu Ile Ala Glu Arg Thr Gly Ala
        275   280   285

Lys Tyr Val Glu Ala Phe Glu Ser Leu Thr Gly Arg Lys Trp Thr
    290   295   300

<210> 29
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      5'-primer for amplification of upstream region
      of URA3 structural gene

<400> 29
ccccgagctc aaaaaaaagg taccaatttc agctccgacg ccggagccca ctacgcctac 60

<210> 30
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      3'-primer for amplification of upstream region
      of URA3 structural gene

<400> 30
gggaagcttc cccagttgta caccaatctt gtcgacag   38

<210> 31
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer Dad1-5 used for destruction of Ogataea
      minuta ADE1 gene

<400> 31
aaaaagcggc cgctcccggt gtcccgcaga aatctttatg cgtagtcttg   50

<210> 32
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer Dad1-3 used for destruction of Ogataea
      minuta ADE1 gene

<400> 32
cccccggatc ctttttttta agcttgttgt actccttcca tgcacttccg gtgatg   56

<210> 33
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer Dad2-5 used for destruction of Ogataea
      minuta ADE1 gene

<400> 33
ttttcacccc gtcaaggatc cctgaacaag gcgaacacga cgaaaacatt tcccccgag   59

<210> 34
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer Dad2-3 used for destruction of Ogataea
      minuta ADE1 gene

<400> 34
tttttgggcc cacctgggtg aagatttgcc agatcaagtt ctcc   44

<210> 35
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DA5 used for confirmation of destruction
      of Ogataea minuta ADE1 gene

<400> 35
gatgcttgcg ccttcaacca catactcctc   30

<210> 36
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DA3 used for confirmation of destruction
      of Ogataea minuta ADE1 gene

<400> 36
aaaagttctt gcacagcctc aatattgacc   30

<210> 37
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DOU5 used for confirmation of destruction
      of Ogataea minuta ADE1 gene

<400> 37
atcgatttcg agtgtttgtc caggtccggg   30

<210> 38
<211> 10
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MOD_RES
<222> (3)
<223> His or Arg

<220>
<221> MOD_RES
<222> (4)
<223> Ile or Val

<400> 38
Pro Gln Xaa Xaa Trp Gln Thr Trp Lys Val
  1   5   10

<210> 39
<211> 11
<212> PRT
<213> Saccharomyces cerevisiae

<400> 39
Trp Tyr Ala Arg Arg Ile Gln Phe Cys Gln Trp
  1   5   10

<210> 40
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer POH5 for amplification of 5'-region of
      Ogataea minuta OCH1 gene

<220>
<221> modified_base
<222> (3)
<223> a, c, g or t

<220>
<221> modified_base
<222> (21)
<223> a, c, g or t

```
<400> 40
ccncarcryr thtggcarac ntggaargt                                    29


<210> 41
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer POH3 for amplification of 3'-region of
      Ogataea minuta OCH1 gene

<220>
<221> modified_base
<222> (19)
<223> a, c, g or t

<220>
<221> modified_base
<222> (22)
<223> a, c, g or t

<220>
<221> modified_base
<222> (25)
<223> a, c, g or t

<400> 41
ccaytgrcar aaytgdatnc knckngcrta cca                               33


<210> 42
<211> 2527
<212> DNA
<213> Ogataea minuta

<400> 42
agatctgttg acactggtca agcgtgtagc caagagaata ggaaacggaa tttcatactg 60
ccggcacaca aggacaataa gggcgtccgg ggctgtcgaa attgtcgaga ccgtagagct 120
attgttacct caataagttg ctctacgatt gtttccgtct ttgacaaagc agtaggcctt 180
tctcaaggtg gtgtacgggt gtttcatttt taatttgcat cgagaacgcg tagtgcgcca 240
atggatctgc aggggctcg gctgattgca ctgaaatttc agcaataaat agctgaggat 300
attcaggcac aacggtacca acggggcagg cttgatcgcg aagcagcagg agaaggcagc 360
gaagtgactg aagagacgag aaggagacga atcagcctac ccctggaacc ataaacaaag 420
tcgagccgtt tttttaggga cagaaaccgt tctggatatt tattcgacgc agagactcgg 480
tagtcatctc tacgttcagc acacaccatg aactatcacg acttgtacga tgatagcaaa 540
cggcagtcgt tgatgcgaaa ggcgcgaaag ttcgctgaga tgaacaagaa gttggtggtg 600
gtggtcattt taacgatgta cgttgtgtcg cgtctggcgt cggttggaag cacgaaacag 660
gagtcgattc caggactcac catgaaagag tcagagttag aggtgaattt taaaacattt 720
ggaatggatc tgcagaagcg gaacgagcta ccggccgcaa gtgcaacgct gagagaaaaa 780
ctatcgtttt acttcccta tgaccctgaa aaaccagtgc ccaaccaaat atggcagacg 840
tggaaagtgg acatcaacga caaatcattc ccgagacact tccgtaagtt ccaagagaca 900
tggccacaac taaacagcgg gtacacgtac catctcattc cagacagtat tgtggacgag 960
ttcatgagga gtcttttgc caatgtccct gaggttattg cagcctacaa catgttaccg 1020
aaaaatatcc tcaaggcgga tttttccgg tatttggtga tttttgcgcg cggtggaact 1080
```

```
tattcggata tcgacacgat ctgcctcaaa ccagtgaacg aatgggccac gtttaacgaa 1140
caaactgtca tttcgcacta tctcaagacc aacggtaaaa cctcgcagtt gccagaagtg 1200
gacccctcca cgcgcaaaac accgatcgga ctcaccattg gaatagaggc cgacccagac 1260
agacccgact ggcacgaatg gtacgctaga cgtattcagt tctgtcaatg gacgatccag 1320
ggcaagcaag gccatcccat gctgcgcgag ttgatcatcc gtatagtgga gcaaactttc 1380
cgcaaagagg ccatgggcaa tttgaaaaaa gtagagggga aggatatggg tggtgacatc 1440
atgcagtgga caggacccgg ggtttttcaca gatacccctgt ttgattatct caataacgtg 1500
gtgagtgacg gaaagctggg agacggttac ggagtcgggt ccaagtactg gaacagtcac 1560
gccaagtaca agctgtctca cattgaggtg gatgccaaca cgagccgat gcactctgac 1620
aagcaaacta tcagctggaa gtccatgagt aagctatcgg agcccctgat tatagatgac 1680
gtgatgatcc tgccaatcac tagcttcagc cccggcgtgg gccagatggg ctcgcattcg 1740
cccgaccacc cgctcgcatt tgtccggcac atgttccagg gcagctggaa accagatgca 1800
gagaagatgt gactgcatat aggaacgcat tttatacagt agatcaagtt aaaagtttga 1860
acttttgcgg ggaagtggtg taagggtgtt tgacgagggc ctgaacccgt gagtcaacgc 1920
gcttggacgg aagaacgggt gcacgccgca tggggctgtt cgttcagttt tgacgctgct 1980
aacgagagag tagcttgcag attgcaatcc cgactgagtc cacccggttg agctagtcac 2040
acgactgcgt cttttctttc tggtgtacgg gtgtcaatac attttcggtt taaaaacgat 2100
aagatgcaac aaggtatctt ctgtagctaa accccacttc tccagacacc ttccaccagc 2160
cgatgactat gacagacagg tttttggagg attacaagaa gtttctcccc aaagcgcacg 2220
atttgagggg cacgcactca cggctttttca cgacggcggg cggggccgat gcggggagtt 2280
tggctgattg gagagagtgg acagatgatt tggtcattc gcaggagtat tacgagctga 2340
aacaggagat caattgtctt gttcttaact accttatcta cgaaggatat gttggtgctg 2400
ttcgagagtt ttcgaaagag ctgggattcg attttatcgt ggaggagttg gaaggaattg 2460
aagaggagaa gggaggccac caagaggacg gagagtacac gaccatgtca gacactgacg 2520
tactagt                                                            2527
```

<210> 43
<211> 434
<212> PRT
<213> Ogataea minuta

<400> 43

```
Met Asn Tyr His Asp Leu Tyr Asp Asp Ser Lys Arg Gln Ser Leu Met
 1               5                   10                  15

Arg Lys Ala Arg Lys Phe Ala Glu Met Asn Lys Lys Leu Val Val Val
            20                  25                  30

Val Ile Leu Thr Met Tyr Val Val Ser Arg Leu Ala Ser Val Gly Ser
        35                  40                  45

Thr Lys Gln Glu Ser Ile Pro Gly Leu Thr Met Lys Glu Ser Glu Leu
    50                  55                  60

Glu Val Asn Phe Lys Thr Phe Gly Met Asp Leu Gln Lys Arg Asn Glu
65                  70                  75                  80

Leu Pro Ala Ala Ser Ala Thr Leu Arg Glu Lys Leu Ser Phe Tyr Phe
                85                  90                  95

Pro Tyr Asp Pro Glu Lys Pro Val Pro Asn Gln Ile Trp Gln Thr Trp
            100                 105                 110

Lys Val Asp Ile Asn Asp Lys Ser Phe Pro Arg His Phe Arg Lys Phe
            115                 120                 125
```

```
Gln Glu Thr Trp Pro Gln Leu Asn Ser Gly Tyr Thr Tyr His Leu Ile
    130             135             140
```

```
Pro Asp Ser Ile Val Asp Glu Phe Met Arg Ser Leu Phe Ala Asn Val
145             150             155                 160
```

```
Pro Glu Val Ile Ala Ala Tyr Asn Met Leu Pro Lys Asn Ile Leu Lys
            165             170             175
```

```
Ala Asp Phe Phe Arg Tyr Leu Val Ile Phe Ala Arg Gly Gly Thr Tyr
            180             185             190
```

```
Ser Asp Ile Asp Thr Ile Cys Leu Lys Pro Val Asn Glu Trp Ala Thr
        195             200             205
```

```
Phe Asn Glu Gln Thr Val Ile Ser His Tyr Leu Lys Thr Asn Gly Lys
    210             215             220
```

```
Thr Ser Gln Leu Pro Glu Val Asp Pro Ser Thr Arg Lys Thr Pro Ile
225             230             235             240
```

```
Gly Leu Thr Ile Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His
            245             250             255
```

```
Glu Trp Tyr Ala Arg Arg Ile Gln Phe Cys Gln Trp Thr Ile Gln Gly
        260             265             270
```

```
Lys Gln Gly His Pro Met Leu Arg Glu Leu Ile Ile Arg Ile Val Glu
        275             280             285
```

```
Gln Thr Phe Arg Lys Glu Ala Met Gly Asn Leu Lys Lys Val Glu Gly
    290             295             300
```

```
Lys Asp Met Gly Gly Asp Ile Met Gln Trp Thr Gly Pro Gly Val Phe
305             310             315             320
```

```
Thr Asp Thr Leu Phe Asp Tyr Leu Asn Asn Val Val Ser Asp Gly Lys
            325             330             335
```

```
Leu Gly Asp Gly Tyr Gly Val Gly Ser Lys Tyr Trp Asn Ser His Ala
            340             345             350
```

```
Lys Tyr Lys Leu Ser His Ile Glu Val Asp Ala Asn Asn Glu Pro Met
    355             360             365
```

```
His Ser Asp Lys Gln Thr Ile Ser Trp Lys Ser Met Ser Lys Leu Ser
    370             375             380
```

```
Glu Pro Leu Ile Ile Asp Asp Val Met Ile Leu Pro Ile Thr Ser Phe
385             390             395             400
```

```
Ser Pro Gly Val Gly Gln Met Gly Ser His Ser Pro Asp His Pro Leu
            405             410             415
```

```
Ala Phe Val Arg His Met Phe Gln Gly Ser Trp Lys Pro Asp Ala Glu
            420             425             430
```

```
Lys Met
```

<210> 44
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DO3 used for confirmation of destruction
      of Ogataea minuta OCH1 gene

<400> 44
ccattgtcag ctccaattct ttgataaacg   30

<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DO5 used for confirmation of destruction
      of Ogataea minuta OCH1 gene

<400> 45
acacttccgt aagttccaag agacatggcc   30

<210> 46
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DO3-2 used for confirmation of destruction
      of Ogataea minuta OCH1 gene

<400> 46
tcaccacgtt attgagataa tcaaacaggg   30

<210> 47
<211> 8
<212> PRT
<213> Saccharomyces cerevisiae

<400> 47
Thr Asn Tyr Leu Asn Ala Gln Tyr
  1   5

<210> 48
<211> 8
<212> PRT
<213> Saccharomyces cerevisiae

<400> 48
Lys Ala Tyr Trp Glu Val Lys Phe
  1   5

<210> 49
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PPA5 for amplification of 5'-region of
      Ogataea minuta PEP4 gene

<220>
<221> modified_base
<222> (3)
<223> a, c, g or t

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (18)
<223> a, c, g or t

<400> 49
acnaaytayy tnaaygcnca rta   23

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PPA3 for amplification of 3'-region of
      Ogataea minuta PEP4 gene

<220>
<221> modified_base
<222> (6)
<223> a, c, g or t

<220>
<221> modified_base
<222> (18)
<223> a, c, g or t

```
<400> 50
aayttnacyt cccartangc ytt                                                    23


<210> 51
<211> 1951
<212> DNA
<213> Ogataea minuta

<220>
<221> modified_base
<222> (35)
<223> a, c, g or t

<400> 51
catatgtatt catcaatcta cagcttttct aatcngtgtg acttcagtca catgatcctc 60
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gctaatcacg aagattttg gatttcctga tctgtagtgt atccatcctg ccttaatcgt 180
tttcgataca tttgttatcc gaattgggaa tggcattagt cgtgcgccac ccgactcgcc 240
accccattc tagtggcaaa caggattgaa agagggctaa aaggtaactt agtgtttat 300
ctctgaatct tccttctgat atcaatcaac aattgttaaa cgattgaaag ttttgaaaca 360
ttcattgaac ttgcgaagcg ctcacacagc atcgttcggt tagcagttac aacagtttag 420
gttttttttcc ccacaaaaag gctcacgctg cctcctcact cttgcctctt ttcttgatga 480
aactctcgct tgcattgctc gcccttggtg gtttccaaga ggcccacgcc aaggttcatc 540
atgcgccaat caagaagact cctgccgcgg aaacttacaa ggacgtgagt ttcggcgact 600
acgtggattc tctgaagggc aagtatgtct ctatgtttgc taagcatgct gcggagtcct 660
cccaaaacgc ctttgtccct tttgttcagg aagtgcaaga cccagagttt actgttcagg 720
agggacacaa ctcccctctc acgaactacg tgaacgctca gtacttcact gagattcaaa 780
ttggtacccc gggccaaccg ttcaaggtca tcctcgacac tggttcgtcc aatttgtggg 840
ttccaggctc ggattgttct tctcttgctt gctacctgca tcagaagtac gaccacgact 900
cttcgtcaac ctacaaggcc aacggctctg aatttgctat cagatacggc tctggttcgc 960
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gaaagatcac ttggttgcca gtgagaagaa aggcttactg ggaggtgaag tttgacggta 1320
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cctctttaat tgctttgcct tcccaattgg ctgagatttt gaactctcaa atcggtgccg 1440
agaagtcctg gtccggccag tacaccattg actgtgaaaa gagagcatct ttgccagacc 1500
tcactttcaa cttttgacggt tacaatttct ctatctccgc gtacgactac actcttgagg 1560
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acgctgttgg attggctaag gccgtttaat ctctagcctt ctagttattg attgctattg 1740
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tggtatgttt attgctttta ttacgtgacc aaatgttggt ttttctttca ccttttactc 1860
tgcactactt cactctttca ttggctttgg aagtacgtta ttttttttcac cctatgtaac 1920
tgaattgcac aaatttaaag attgctctag a                                     1951


<210> 52
<211> 410
<212> PRT
<213> Ogataea minuta
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<400> 52

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Met Lys Leu Ser Leu Ala Leu Leu Ala Leu Gly Gly Phe Gln Glu Ala
 1               5                  10                  15

His Ala Lys Val His His Ala Pro Ile Lys Lys Thr Pro Ala Ala Glu
            20              25                  30

Thr Tyr Lys Asp Val Ser Phe Gly Asp Tyr Val Asp Ser Leu Lys Gly
        35                  40                  45

Lys Tyr Val Ser Met Phe Ala Lys His Ala Ala Glu Ser Ser Gln Asn
    50                  55                  60

Ala Phe Val Pro Phe Val Gln Glu Val Gln Asp Pro Glu Phe Thr Val
65                  70                  75                  80

Gln Glu Gly His Asn Ser Pro Leu Thr Asn Tyr Val Asn Ala Gln Tyr
            85                  90                  95

Phe Thr Glu Ile Gln Ile Gly Thr Pro Gly Gln Pro Phe Lys Val Ile
            100                 105                 110

Leu Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Gly Ser Asp Cys Ser
        115                 120                 125

Ser Leu Ala Cys Tyr Leu His Gln Lys Tyr Asp His Asp Ser Ser Ser
    130                 135                 140

Thr Tyr Lys Ala Asn Gly Ser Glu Phe Ala Ile Arg Tyr Gly Ser Gly
145                 150                 155                 160

Ser Leu Glu Gly Phe Val Ser Gln Asp Thr Leu Thr Leu Gly Asp Leu
            165                 170                 175

Ile Ile Pro Lys Gln Asp Phe Ala Glu Ala Thr Ser Glu Pro Gly Leu
            180                 185                 190

Ala Phe Ala Phe Gly Lys Phe Asp Gly Ile Leu Gly Leu Ala Tyr Asp
        195                 200                 205

Thr Ile Ser Val Asp Lys Ile Val Pro Pro Ile Tyr Asn Ala Leu Asn
210                 215                 220

Leu Gly Leu Leu Asp Glu Pro Gln Phe Ala Phe Tyr Leu Gly Asp Thr
225                 230                 235                 240

Ala Lys Ser Glu Ala Asp Gly Gly Val Ala Thr Phe Gly Gly Val Asp
            245                 250                 255

Glu Thr Lys Tyr Asp Gly Lys Ile Thr Trp Leu Pro Val Arg Arg Lys
            260                 265                 270

Ala Tyr Trp Glu Val Lys Phe Asp Gly Ile Ala Leu Gly Asp Glu Tyr
        275                 280                 285

Ala Thr Leu Asp Gly Tyr Gly Ala Ala Ile Asp Thr Gly Thr Ser Leu
    290                 295                 300
```

```
Ile Ala Leu Pro Ser Gln Leu Ala Glu Ile Leu Asn Ser Gln Ile Gly
305                 310             315                 320

Ala Glu Lys Ser Trp Ser Gly Gln Tyr Thr Ile Asp Cys Glu Lys Arg
                325             330             335

Ala Ser Leu Pro Asp Leu Thr Phe Asn Phe Asp Gly Tyr Asn Phe Ser
                340             345             350

Ile Ser Ala Tyr Asp Tyr Thr Leu Glu Val Ser Gly Ser Cys Ile Ser
            355             360             365

Ala Phe Thr Pro Met Asp Phe Pro Ala Pro Ile Gly Pro Leu Ala Ile
        370             375             380

Ile Gly Asp Ala Phe Leu Arg Lys Tyr Tyr Ser Val Tyr Asp Leu Gly
385             390             395                 400

Lys Asp Ala Val Gly Leu Ala Lys Ala Val
                405             410
```

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<210> 53
<211> 11
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MOD_RES
<222> (2)
<223> Gly or Leu

<400> 53
Asp Xaa Asn Gly His Gly Thr His Cys Ala Gly
  1               5                 10


<210> 54
<211> 11
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MOD_RES
<222> (6)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (9)
<223> Val or Ile

<220>
<221> MOD_RES
<222> (10)
<223> Ala or Val
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<400> 54
Gly Thr Ser Met Ala Xaa Pro His Xaa Xaa Gly
  1               5                   10


<210> 55
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PPB5 for amplification of 5'-region of
      Ogataea minuta PRB1 gene

<220>
<221> modified_base
<222> (6)
<223> a, c, g or t

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (18)
<223> a, c, g or t

<220>
<221> modified_base
<222> (21)
<223> a, c, g or t

<220>
<221> modified_base
<222> (30)
<223> a, c, g or t

<400> 55
gaybknaayg gncayggnac ncaytgykcn gg                    32


<210> 56
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PPB3 for amplification of 3'-region of
      Ogataea minuta PRB1 gene

<220>
<221> modified_base
<222> (3)
<223> a, c, g or t
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<220>
<221> modified_base
<222> (6)
<223> a, c, g or t

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (15)
<223> a, c, g or t

<220>
<221> modified_base
<222> (18)
<223> a, c, g or t

<220>
<221> modified_base
<222> (24)
<223> a, c, g or t

<220>
<221> modified_base
<222> (27)
<223> a, c, g or t

<220>
<221> modified_base
<222> (30)
<223> a, c, g or t

<400> 56
ccnrcnayrt gnggnwsngc catnwsngtn cc                                    32


<210> 57
<211> 2214
<212> DNA
<213> Ogataea minuta

<400> 57
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cagatcccaa  atttgccacc  agactaaatt  ggggcattct  ggtgagggaa  tagggaaat  180
aagagggtgt  tttgacgttt  catatacatt  gctctttctt  ttcttggacg  gttagcggta  240
ttgccataga  ttatcttgcg  cagttcagca  tccttaggag  ttattctttc  ttgtaggtct  300
tttttcagaa  cagaaaaatc  gccaatcaca  gaaagattca  gtcctaattg  aagccttatc  360
ttatcttatc  tcacctcaac  cacttgaacc  aaaatgaagt  tatcccagtc  tgctgcggtg  420
gctattctgt  cttcgttggc  agcagtggag  gccttggtca  tcccgttatt  tgacgacttg  480
ccagcagagt  ttgcccttgt  tccaatggat  gcgaaagcgg  aagtcatttc  tgacgttcct  540
gtcgactcgg  ccattagtga  tgctcctatc  gcggcactaa  atgatgctcc  aagccctctc  600
gtcacatcgc  tgatcgcatc  tcaaaatttg  attccaaact  cttatattgt  cgttttcaag  660
aatggcctag  cttccggggc  agttgacttc  cacatggagt  ggctcaagga  aacgcactcc  720
```

```
caaaccctgg ctgctttgtc taaggacatg ccagcagaag aattggccgc cgaaggtttc 780
gtttccgaaa gcattgatct tactgaggtg tttagcatct ccgatttgtt cagtggatat 840
accggatact ccccggagaa ggtggttgac ctcatcagaa gacaccctga cgtggcgttc 900
gttgagcagg actcgagagt tttcgccgat aagtcgtcta ctcaaaacgg tgctccttgg 960
ggtttgtcta gaatctctca cagagagcct ctcagtctcg gcaatttcaa cgagtacgtt 1020
tacgacgatc ttgctggaga tggcgtcacg gcttatgtca ttgataccgg tatcaatgtg 1080
aagcacgagc agttcggtgg cagagcagag tggggtaaga ccatcccaac cggtgatgat 1140
gatattgacg gaaacggtca cggtactcac tgcgctggta caattggctc ggaagattat 1200
ggagtttcta gaactccaa aattgtcgca gtgaaggttt tgagatctaa cggttctggt 1260
tccatgtctg acgtgatcaa gggtgttgaa ttcgctgcaa atgatcacgt tgccaagtct 1320
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tctcctgctc ttgacttggc tgtcaatgcc gctgtcaaag ctggtttaca ctttgctgtt 1440
gccgctggta acgacaatgc tgacgcatgc aactattctc ctgctgctgc agagaacgca 1500
gtcactgttg gtgcgtccac tttgtctgac tctagagctt acttttccaa ctatggtaaa 1560
tgtgttgaca tttttgctcc gggcttgaac atcctttcca cctacatagg ttctgacact 1620
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tactttttga gcttgcaacc agaatcgtcc tcgttgtttt cttcggcagc tatctcccct 1740
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tcggacggaa ccccaaatat tctcatttac aacggtgctg gcaagaacat cagtgacttc 1860
tgggcgtttg aagacgaggc ctcggccaag tccgacttga agaaggctgt cgatattgcc 1920
acaagtgttg acttagacct gcaagatatc aaggagaagt tcaaccatat tttggaggag 1980
gtcgccgaag aggttgctga tttgttcgat taggtttcta acaattcagt gatcttgtct 2040
ttactgtggt ttcggaaact gggtttagac agcggtcctg ttactcatat tgcgcttgat 2100
cgcttttcct tttttttctg ttgtttggag tgtttgtttt tctggataat gtggttagtt 2160
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```

<210> 58
<211> 539
<212> PRT
<213> Ogataea minuta

<400> 58
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Met Lys Leu Ser Gln Ser Ala Ala Val Ala Ile Leu Ser Ser Leu Ala
 1               5                  10                  15

Ala Val Glu Ala Leu Val Ile Pro Leu Phe Asp Asp Leu Pro Ala Glu
            20                  25                  30

Phe Ala Leu Val Pro Met Asp Ala Lys Ala Glu Val Ile Ser Asp Val
          35                  40                  45

Pro Val Asp Ser Ala Ile Ser Asp Ala Pro Ile Ala Ala Leu Asn Asp
     50                  55                  60

Ala Pro Ser Pro Leu Val Thr Ser Leu Ile Ala Ser Gln Asn Leu Ile
 65                  70                  75                  80

Pro Asn Ser Tyr Ile Val Val Phe Lys Asn Gly Leu Ala Ser Gly Ala
                 85                  90                  95

Val Asp Phe His Met Glu Trp Leu Lys Glu Thr His Ser Gln Thr Leu
            100                 105                 110

Ala Ala Leu Ser Lys Asp Met Pro Ala Glu Glu Leu Ala Ala Glu Gly
          115                 120                 125
```

```
Phe Val Ser Glu Ser Ile Asp Leu Thr Glu Val Phe Ser Ile Ser Asp
    130             135             140
```

```
Leu Phe Ser Gly Tyr Thr Gly Tyr Phe Pro Glu Lys Val Val Asp Leu
145             150             155             160
```

```
Ile Arg Arg His Pro Asp Val Ala Phe Val Glu Gln Asp Ser Arg Val
            165             170             175
```

```
Phe Ala Asp Lys Ser Ser Thr Gln Asn Gly Ala Pro Trp Gly Leu Ser
            180             185             190
```

```
Arg Ile Ser His Arg Glu Pro Leu Ser Leu Gly Asn Phe Asn Glu Tyr
        195             200             205
```

```
Val Tyr Asp Asp Leu Ala Gly Asp Gly Val Thr Ala Tyr Val Ile Asp
    210             215             220
```

```
Thr Gly Ile Asn Val Lys His Glu Gln Phe Gly Gly Arg Ala Glu Trp
225             230             235             240
```

```
Gly Lys Thr Ile Pro Thr Gly Asp Asp Asp Ile Asp Gly Asn Gly His
            245             250             255
```

```
Gly Thr His Cys Ala Gly Thr Ile Gly Ser Glu Asp Tyr Gly Val Ser
            260             265             270
```

```
Lys Asn Ser Lys Ile Val Ala Val Lys Val Leu Arg Ser Asn Gly Ser
            275             280             285
```

```
Gly Ser Met Ser Asp Val Ile Lys Gly Val Glu Phe Ala Ala Asn Asp
    290             295             300
```

```
His Val Ala Lys Ser Lys Ala Lys Lys Asp Gly Phe Lys Gly Ser Thr
305             310             315             320
```

```
Ala Asn Met Ser Leu Gly Gly Gly Lys Ser Pro Ala Leu Asp Leu Ala
            325             330             335
```

```
Val Asn Ala Ala Val Lys Ala Gly Leu His Phe Ala Val Ala Ala Gly
            340             345             350
```

```
Asn Asp Asn Ala Asp Ala Cys Asn Tyr Ser Pro Ala Ala Ala Glu Asn
            355             360             365
```

```
Ala Val Thr Val Gly Ala Ser Thr Leu Ser Asp Ser Arg Ala Tyr Phe
    370             375             380
```

```
Ser Asn Tyr Gly Lys Cys Val Asp Ile Phe Ala Pro Gly Leu Asn Ile
385             390             395             400
```

```
Leu Ser Thr Tyr Ile Gly Ser Asp Thr Ala Thr Ala Thr Leu Ser Gly
            405             410             415
```

```
Thr Ser Met Ala Ser Pro His Val Cys Gly Leu Leu Thr Tyr Phe Leu
            420             425             430
```

Ser Leu Gln Pro Glu Ser Ser Ser Leu Phe Ser Ser Ala Ala Ile Ser
        435   440   445

Pro Ala Gln Leu Lys Lys Asn Leu Ile Lys Phe Gly Thr Lys Asn Val
    450   455   460

Leu Ser Glu Ile Pro Ser Asp Gly Thr Pro Asn Ile Leu Ile Tyr Asn
465   470   475   480

Gly Ala Gly Lys Asn Ile Ser Asp Phe Trp Ala Phe Glu Asp Glu Ala
            485   490   495

Ser Ala Lys Ser Asp Leu Lys Lys Ala Val Asp Ile Ala Thr Ser Val
            500   505   510

Asp Leu Asp Leu Gln Asp Ile Lys Glu Lys Phe Asn His Ile Leu Glu
        515   520   525

Glu Val Ala Glu Glu Val Ala Asp Leu Phe Asp
    530   535

<210> 59
<211> 9
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MOD_RES
<222> (1)
<223> His or Asn

<220>
<221> MOD_RES
<222> (5)
<223> Val or Thr

<400> 59
Xaa Tyr Asp Trp Xaa Phe Leu Asn Asp
  1   5

<210> 60
<211> 12
<212> PRT
<213> Saccharomyces cerevisiae

<400> 60
Tyr Asn Leu Cys His Phe Trp Ser Asn Phe Glu Ile
  1   5   10

<210> 61
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
    primer PKR5 for amplification of 5'-region of
    Ogataea minuta KTR1 gene

<220>
<221> modified_base
<222> (15)
<223> a, c, g or t

<220>
<221> modified_base
<222> (21)
<223> a, c, g or t

<400> 61
maytaygayt ggrynttyyt naayga   26

<210> 62
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
    primer PKR3 for amplification of 3'-region of
    Ogataea minuta KTR1 gene

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (27)
<223> a, c, g or t

<400> 62
atytcraart tnswccaraa rtgrcanarr ttrta   35

<210> 63
<211> 1930
<212> DNA
<213> Ogataea minuta

<400> 63
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acaatggcta gagcgaatgc gaggctgatc cggtttgcaa tctttgctac cgtgttggtt 180
ttatgtggat acattttatc caagggctcg tctacttcgt atacgatttc gacgccagag 240
tccggctcga gttccagtgg cactgttgct aatactgaga aatctgccct cgcagtgggt 300
gagaaaagcg ttgcaggcgc agccgagaaa agcgttcctg cagctgacgt cccagatgga 360
aaggtgaagg ccacttttgt ctctttggcc agaaaccagg atctgtggga gctggtgaac 420
tcgatcagac aggtcgaaga ccgttcaac aacaagtatc attacgattg ggtgttcttg 480
aacgacgcgg aattcaacga cgagttcaag aaggtgacct ctcaggtctg ttcgggtaag 540

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accaagtatg gtgtcattcc aaaggaacag tggagcttcc cttcgtggat cgacactgat 600
aaggctgctg ccaccagaga gcaaatgaga aaggacaaga tcatctacgg agactccatc 660
tcgtacagac acatgtgcag atacgagtcg ggattcttct tcaaacaccc agaactcgca 720
gagtacgagt actactggag agtggagcca agcatcaaga tctactgtga cattgactac 780
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tacaatggat gtcacttctg gtctaacttc gaggtcggct cgctcgagtt ctggagaggc 1020
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gctgtcagag aggccaagaa ctgtgtctgc aaccaagccg acgacttcac cttccagcac 1260
tactcctgta cccctaagtt ttaccaggag atgggtttga aaaagcctgc taactgggag 1320
cagtacatcc attagttgac ccaggccacg ggttgattc gcctggttgt tttttgtttt 1380
tacaagtctt tcaatactaa attagctgga ttcaagtgat acgagatgat tttcatctcc 1440
ggggtttctg taatttttgt ttcgagaaaa ataaatctac aaaaaaacgt gccagatact 1500
tgtctcccgg gggcaaacaa cgtgctctct ctgctactaa gtgttttgtt tctgtccaca 1560
acgcccgcag gtaaacgcaa tgtccgatac agattctgag tcagtctcga cgatcacaca 1620
gatgagcttc gagaacgttc tcgaggttct agaagactct gcgtctgagt gctccaagaa 1680
caaggacttc ctctccttct cgacgatcat cgacgtccat ctgggtgatc tttccattta 1740
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ccaattggtt tacgaggtag gatgggactt accaccgatc atattcagct tcctggactc 1860
tgaatcttcg cccagtgagg ggctgatgaa cagcaaggtc acggttcttt tcttgaagct 1920
gtttgagctc                                                       1930
```

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<210> 64
<211> 403
<212> PRT
<213> Ogataea minuta

<400> 64
Met Ala Arg Ala Asn Ala Arg Leu Ile Arg Phe Ala Ile Phe Ala Thr
1               5                   10                  15

Val Leu Val Leu Cys Gly Tyr Ile Leu Ser Lys Gly Ser Ser Thr Ser
            20                  25                  30

Tyr Thr Ile Ser Thr Pro Glu Ser Gly Ser Ser Ser Ser Gly Thr Val
        35                  40                  45

Ala Asn Thr Glu Lys Ser Ala Leu Ala Val Gly Glu Lys Ser Val Ala
    50                  55                  60

Gly Ala Ala Glu Lys Ser Val Pro Ala Ala Asp Val Pro Asp Gly Lys
65                  70                  75                  80

Val Lys Ala Thr Phe Val Ser Leu Ala Arg Asn Gln Asp Leu Trp Glu
                85                  90                  95

Leu Val Asn Ser Ile Arg Gln Val Glu Asp Arg Phe Asn Asn Lys Tyr
            100                 105                 110

His Tyr Asp Trp Val Phe Leu Asn Asp Ala Glu Phe Asn Asp Glu Phe
        115                 120                 125

Lys Lys Val Thr Ser Gln Val Cys Ser Gly Lys Thr Lys Tyr Gly Val
    130                 135                 140
```

Ile Pro Lys Glu Gln Trp Ser Phe Pro Ser Trp Ile Asp Thr Asp Lys
145   150   155   160

Ala Ala Ala Thr Arg Glu Gln Met Arg Lys Asp Lys Ile Ile Tyr Gly
                165   170   175

Asp Ser Ile Ser Tyr Arg His Met Cys Arg Tyr Glu Ser Gly Phe Phe
                180   185   190

Phe Lys His Pro Glu Leu Ala Glu Tyr Glu Tyr Tyr Trp Arg Val Glu
            195   200   205

Pro Ser Ile Lys Ile Tyr Cys Asp Ile Asp Tyr Asp Ile Phe Lys Phe
        210   215   220

Met Lys Asp Asn Lys Lys Ser Tyr Gly Trp Thr Ile Ser Leu Pro Glu
225   230   235   240

Tyr Lys Glu Thr Ile Pro Thr Leu Trp Lys Thr Thr Arg Asp Phe Met
                245   250   255

Lys Glu Asn Pro Gln Tyr Val Ala Gln Asp Asn Leu Ile Asn Phe Ile
                260   265   270

Ser Asp Asp Gly Gly Ser Ser Tyr Asn Gly Cys His Phe Trp Ser Asn
            275   280   285

Phe Glu Val Gly Ser Leu Glu Phe Trp Arg Gly Glu Ala Tyr Thr Lys
            290   295   300

Tyr Phe Glu Ala Leu Asp Gln Ala Gly Gly Phe Phe Tyr Glu Arg Trp
305   310   315   320

Gly Asp Ala Pro Ile His Ser Ile Ala Val Ala Leu Phe Met Pro Lys
                325   330   335

Asp Glu Val His Phe Phe Asp Asp Val Gly Tyr Phe His Asn Pro Phe
            340   345   350

His Asn Cys Pro Ile Asp Asn Ala Val Arg Glu Ala Lys Asn Cys Val
            355   360   365

Cys Asn Gln Ala Asp Asp Phe Thr Phe Gln His Tyr Ser Cys Thr Pro
            370   375   380

Lys Phe Tyr Gln Glu Met Gly Leu Lys Lys Pro Ala Asn Trp Glu Gln
385   390   395   400

Tyr Ile His

<210> 65
<211> 10
<212> PRT
<213> Saccharomyces cerevisiae

<400> 65
Thr Ser Trp Val Leu Trp Leu Asp Ala Asp
 1   5   10

<210> 66
<211> 10
<212> PRT
<213> Saccharomyces cerevisiae

<400> 66
Glu Thr Glu Gly Phe Ala Lys Met Ala Lys
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<210> 67
<211> 29
<212> DNA
<213> Artificial Sequence

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      primer PMN5 for amplification of 5'-region of
      Ogataea minuta MNN9 gene

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<223> a, c, g or t

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<223> a, c, g or t

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<222> (12)
<223> a, c, g or t

<220>
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<222> (15)
<223> a, c, g or t

<220>
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<223> a, c, g or t

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<400> 67
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<211> 29
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<213> Artificial Sequence

<220>
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      primer PMN3 for amplification of 3'-region of
      Ogataea minuta MNN9 gene

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<223> a, c, g or t

<220>
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<223> a, c, g or t

<400> 68
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<210> 69
<211> 2221
<212> DNA
<213> Ogataea minuta

<400> 69
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t                                                                   2221
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<210> 70
<211> 367
<212> PRT
<213> Ogataea minuta

<400> 70

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Met Leu Lys Gly Val Leu Lys His Pro Leu Val His Gln Ile Arg Arg
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Lys Pro Val Lys Val Leu Val Pro Val Phe Gly Leu Ala Val Leu Leu
             20                  25                  30

Phe Leu Val Phe Gly Gly Ser Ser Ser Asn Arg Lys Thr Asn Ser Pro
         35                  40                  45

Tyr Ser Tyr Lys Arg Asn Asn Arg Asp Glu Val Ile Pro Arg Asn Leu
     50                  55                  60

Pro Ala Asp His Ile Ser His Tyr Asp Leu Asn Asn Leu Ala Ser Thr
 65                  70                  75                  80

Pro Met Ala Ala Tyr Asn Lys Glu Arg Val Leu Ile Leu Thr Pro Met
                 85                  90                  95

Ala Lys Phe Leu Asp Gly Tyr Trp Asp Asn Leu Leu Lys Leu Thr Tyr
                100                 105                 110

Pro Arg Asp Leu Ile Glu Leu Gly Phe Ile Val Pro Arg Thr Ala Glu
             115                 120                 125

Gly Asp Gln Ala Leu Lys Lys Leu Glu His Ala Val Lys Ile Ile Gln
     130                 135                 140

Asn Pro Lys Asn Thr Lys Glu Pro Lys Phe Ala Lys Val Thr Ile Leu
145                 150                 155                 160
```

```
Arg Gln Asp Asn Glu Ser Leu Ser Ser Gln Ser Glu Lys Asp Arg His
            165                 170                 175

Ala Phe Lys Val Gln Lys Glu Arg Arg Ala Gln Met Ala Thr Ala Arg
            180                 185                 190

Asn Ser Leu Leu Phe Thr Thr Ile Gly Pro Tyr Thr Ser Trp Val Leu
            195                 200                 205

Trp Leu Asp Ser Asp Ile Val Glu Ser Pro His Thr Leu Ile Gln Asp
    210                 215                 220

Leu Val Ser His Asp Lys Pro Val Ile Ala Ala Asn Cys Tyr Gln Arg
225                 230                 235                 240

Tyr Tyr Asp Glu Asp Lys Lys Glu Asp Ser Ile Arg Pro Tyr Asp Phe
            245                 250                 255

Asn Asn Trp Ile Glu Ser Glu Glu Gly Leu Arg Ile Ala Ser Thr Met
            260                 265                 270

Ser Asp Asp Glu Ile Ile Val Glu Ala Tyr Ala Glu Ile Ala Thr Tyr
            275                 280                 285

Arg Pro Leu Met Gly His Phe Tyr Asp Pro Asn Gly Asp Leu Gly Thr
    290                 295                 300

Glu Met Gln Leu Asp Gly Val Gly Gly Thr Cys Leu Met Val Lys Ala
305                 310                 315                 320

Asp Val His Arg Asp Gly Ala Met Phe Pro Asn Phe Pro Phe Tyr His
            325                 330                 335

Leu Ile Glu Thr Glu Gly Phe Ala Lys Met Ala Lys Arg Leu Gly Tyr
            340                 345                 350

Gln Val Phe Gly Leu Pro Asn Tyr Leu Val Phe His Tyr Asn Glu
            355                 360                 365
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<210> 71
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DMN5

<400> 71
agatgaggtg attccacgta atttgccagc   30

<210> 72
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DMN3

<400> 72
ttttgattgt catctatttc gcacaccctg   30

<210> 73
<211> 12
<212> PRT
<213> Pichia pastoris

<400> 73
Gly Gly Gly Ser Ser Ile Asn Phe Met Met Tyr Thr
  1   5   10

<210> 74
<211> 10
<212> PRT
<213> Pichia pastoris

<400> 74
Asp Met Trp Pro Met Val Trp Ala Tyr Lys
  1   5   10

<210> 75
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PAX5 for amplification of 5'-region of
      Ogataea minuta AOX1 gene

<220>
<221> modified_base
<222> (3)
<223> a, c, g or t

<220>
<221> modified_base
<222> (6)
<223> a, c, g or t

<220>
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<222> (9)
<223> a, c, g or t

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

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<220>
<221> modified_base
<222> (15)
<223> a, c, g or t

<400> 75
ggnggnggnw snwsnathaa yttyatgatg tayac                              35


<210> 76
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
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      primer PAX3 for amplification of 3'-region of
      Ogataea minuta AOX1 gene

<220>
<221> modified_base
<222> (6)
<223> a, c, g or t

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (18)
<223> a, c, g or t

<400> 76
ttrtangccc anaccatngg ccacatrtc                                    29


<210> 77
<211> 5817
<212> DNA
<213> Ogataea minuta

<400> 77
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ggctagcgat agaatgtatc agtgttatta gtggctctag gagtagaaaa caatagaata 240
aagatccgaa gaaagggagc aagaaggcca cgccagacgt tctagtaggt agcccaatcg 300
tcaatgtagc tgttcaggtc tttcaacagg ttcttggtct cgtctggact ggagatccaa 360
caagtcgttg ctgcggttcg actggcatag tcgttggcgc cgagggagct gaactggtcg 420
ccgacgtgca gggtgttttc gggcttgatg gttcggttgt cgttgcagct gaggaactct 480
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<210> 78
<211> 663
<212> PRT
<213> Ogataea minuta

<400> 78

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Cys Gly Cys Ala Ile Ala Gly Arg Leu Gly Asn Leu Asp Pro Asp Val
             20                  25                  30

Thr Val Ala Leu Ile Glu Gly Gly Glu Asn Asn Ile Asn Asn Pro Trp
         35                  40                  45

Val Tyr Leu Pro Gly Val Tyr Pro Arg Asn Met Arg Leu Asp Ser Lys
     50                  55                  60

Thr Ala Thr Phe Tyr Asn Ser Arg Pro Ser Lys His Leu Asn Gly Arg
 65                  70                  75                  80

Arg Ala Ile Val Pro Cys Ala Asn Ile Leu Gly Gly Gly Ser Ser Ile
                 85                  90                  95

Asn Phe Leu Met Tyr Thr Arg Ala Ser Ala Ser Asp Tyr Asp Asp Trp
                100                 105                 110

Glu Gln Glu Gly Trp Thr Thr Asp Glu Leu Leu Pro Leu Met Lys Lys
            115                 120                 125
```

Leu Glu Thr Tyr Gln Arg Pro Cys Asn Asn Arg Glu Val His Gly Phe
    130   135   140

Asp Gly Pro Ile Lys Val Ser Phe Gly Asn Tyr Thr Tyr Pro Thr Ala
145   150   155   160

Gln Asp Phe Leu Arg Ala Cys Glu Ser Gln Gly Ile Pro Phe Asn Asp
        165   170   175

Asp Leu Glu Asp Leu Lys Ala Ser His Gly Ala Glu Tyr Trp Leu Lys
        180   185   190

Trp Ile Asn Arg Asp Leu Gly Arg Arg Ser Asp Ser Ala His Ala Tyr
        195   200   205

Ile His Pro Thr Met Arg Asn Lys Ser Asn Leu Phe Leu Ile Thr Ser
      210   215   220

Thr Lys Ala Asp Lys Val Ile Ile Glu Asn Gly Val Ala Val Gly Val
225   230   235   240

Arg Thr Val Pro Met Lys Pro Val Glu Thr Lys Asn Pro Pro Ser Arg
        245   250   255

Ile Phe Lys Ala Arg Lys Gln Ile Val Val Ser Cys Gly Thr Ile Ser
        260   265   270

Ser Pro Leu Val Leu Gln Arg Ser Gly Ile Gly Ala Ala His Lys Leu
        275   280   285

Arg Gln Ala Gly Ile Lys Pro Ile Val Asp Leu Pro Gly Val Gly Glu
      290   295   300

Asn Phe Gln Asp His Tyr Cys Phe Phe Thr Pro Tyr Tyr Ser Lys Pro
305   310   315   320

Glu Val Pro Thr Phe Asp Asp Phe Val Arg Gly Asp Pro Val Ala Gln
        325   330   335

Lys Ser Ala Phe Asp Gln Trp Tyr Ser Asn Lys Asp Gly Pro Leu Thr
        340   345   350

Thr Asn Gly Ile Glu Ala Gly Val Lys Ile Arg Pro Thr Asp Glu Glu
      355   360   365

Leu Ala Thr Ala Asp Asp Asp Phe Ile Gln Gly Tyr His Glu Tyr Phe
      370   375   380

Asp Asn Lys Pro Asp Lys Pro Leu Met His Tyr Ser Val Ile Ser Gly
385   390   395   400

Phe Phe Gly Asp His Thr Lys Ile Pro Asn Gly Lys Phe Phe Thr Met
        405   410   415

Phe His Phe Leu Glu Tyr Pro Phe Ser Arg Gly Phe Val Tyr Ala Val
        420   425   430

```
Ser Pro Asp Pro Tyr Glu Ala Pro Asp Phe Asp Pro Gly Phe Leu Asn
        435             440             445

Asp Ser Arg Asp Met Trp Pro Met Val Trp Ser Tyr Lys Lys Ser Arg
        450             455             460

Gln Thr Ala Arg Arg Met Glu Ser Phe Ala Gly Glu Val Thr Ser His
465             470             475             480

His Pro Leu Tyr Pro Val Asp Ser Pro Ala Arg Ala Lys Asp Leu Asp
            485             490             495

Leu Glu Thr Cys Lys Ala Phe Ala Gly Pro Asn His Phe Thr Ala Asn
            500             505             510

Leu Tyr His Gly Ser Trp Thr Val Pro Ile Glu Lys Pro Thr Pro Lys
        515             520             525

Asn Asp Ser His Val Thr Cys Asn Gln Val Glu Ile Phe Ser Asp Ile
        530             535             540

Asp Tyr Ser Ala Glu Asp Asp Glu Ala Ile Val Lys Tyr Ile Lys Glu
545             550             555             560

His Thr Glu Thr Thr Trp His Cys Leu Gly Thr Cys Ser Met Ala Pro
            565             570             575

Gln Glu Gly Ser Lys Ile Ala Pro Lys Gly Gly Val Val Asp Ala Arg
        580             585             590

Leu Asn Val Tyr Glu Val Lys Asn Leu Lys Val Ala Asp Leu Ser Ile
        595             600             605

Cys Pro Asp Asn Val Gly Cys Asn Thr Tyr Ser Thr Ala Leu Leu Ile
    610             615             620

Gly Glu Lys Ala Ala Thr Leu Val Ala Glu Asp Leu Gly Tyr Ser Gly
625             630             635             640

Ser Asp Leu Ala Met Thr Ile Pro Asn Phe Lys Leu Gly Thr Tyr Glu
            645             650             655

Glu Lys Gly Leu Ala Arg Phe
            660
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<210> 79
<211> 2348
<212> DNA
<213> Ogataea minuta

<400> 79
aagctttctt tcgcaaacag ctcttggta gaggagaata gagtgcccag ctgataaaga  60
aggcgcactt taaaagataa tctacatcca gaaaaataaa aaaataaaac tgaaccggca  120
tttgcgatta cgtaagccac aaaatttcag gaaactcgta caagatcagg ttggcgaggg  180
ggctagcgat agaatgtatc agtgttatta gtggctctag gagtagaaaa caatagaata  240
aagatccgaa gaaagggagc aagaaggcca cgccagacgt tctagtaggt agcccaatcg  300
tcaatgtagc tgttcaggtc tttcaacagg ttcttggtct cgtctggact ggagatccaa  360
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```
caagtcgttg ctgcggttcg actggcatag tcgttggcgc cgagggagct gaactggtcg 420
ccgacgtgca gggtgttttc gggcttgatg gttcggttgt cgttgcagct gaggaactct 480
tggaggattt tcaccccgta ggacttgtcg ccaatatcga cccagatgtc cgagcctccg 540
ttgaaagcgc accatctgat tttcttagag gaagggaagt ggcggagacg tttgtctacg 600
cgcagaacca cctcttccag ctgctcgcga acgagtttgt agccttcttt ggggaccagt 660
ccaacggcac gctcctttct gatgatgatg gcatgcaatg aaagtttctt gatcaggtcc 720
gagaagatct cctgcgcaaa gtccagggtc cggatgatgt cttcctcgga ccagtcgagc 780
atgttttcaa gcagccattt gtctttggag aagaactcga gtccgccaag ctcgttggag 840
tagcggaata ggtagtttgc ttcgcctccc atcaccagaa cgttctggcg ctgtctgtcg 900
gtgagctttg gggtggtctt cacctcgtct atgagcccct tgagtcgggc gtagtacttg 960
gagccgtcgg agtagcccgc ggcagtgacg atgccgacat agaggtcttt ggcgagcagc 1020
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gagggcgcta caagtctcct tttgctgatt gtgcggcgtc cgtcctcgat gtagaacgcc 1260
ttctccaggg gcaatcgggt gaagaaacag ccaacggaag gcaccaattg gaccaatctg 1320
gacatttcag gcattcccgc ctgggtcatc tcgatgttgt cgttgatcag cagctcgagg 1380
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atccactcaa tcagtccgtc tcggcggtgc tccttgagcg cgtactcgac tctgtatctg 1560
gttgtcattt gcgggagggg tgtaaagcag ctcagccggt gactgtgcaa ggacgaacgg 1620
ttcctacttg aatgctaggc tggctaattg ggtatggcac aaacggcaca aacggcagat 1680
gactgcaaat gacgacggta aacagaatcc actcagctgg cactaactgg gtgtagacta 1740
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aaactgcgta taaatagcta cttccatctc ctacttgttg caccattgcc atagtaagaa 2280
aagaagcaga tcactcaact tgttcaaaga ctcttgtgtt ctgttacgac ttacgactta 2340
cgaaaaaa                                                        2348
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<210> 80
<211> 802
<212> DNA
<213> Ogataea minuta

<400> 80
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ctacttgatg atgtatgacg agtgaagatt gtgttttttt ctctctatag ttttgactgt 120
aatgaaaata gtctacatga atgaaagaga tagctgacca atacggggcg tctggtcacg 180
tgatgtatca cgtgatcttt aagttttcga aatgactaaa tttataacga aaaaaagagt 240
ctaaatgaaa aaaaatcgat ctctgccaaa gactcatcga taggctaact caggaagcat 300
tccgagcaac gcataatgcc ctcaaccaca gtctcagaga tgcgcaaaaa ggtgctgatg 360
atcgacaatt acgactcgtt cacatggaac ttgtacgagt atctttgtca agagggagcc 420
gatgtcgagg tctatcgtaa cgacaagatc acaattgaag aaatcgagga aatgaagcct 480
gacattatag tgatttcgcc aggccccgga catccgagat cggactctgg tatctctcga 540
aagactattg agattttcaa gggccggatt cctgtttttg gagtgtgcat gggccaacag 600
tgcatttacg aggttttcgg gggagacgtt gagtacgctg gtgaaattgt tcacggaaaa 660
acctcttctg tgacccacga caatcgtgga gtcttcaaga acgttccgca gggagttgct 720
gtgacgagat accattcgtt ggctggaacg ctaaaaactt gcccagcga gttggaggtg 780
actgcccgta ccactaacgg ta                                        802
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<210> 81
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer OAP5 for production of an expression
      cassette with AOX1 gene promoter and terminator

<400> 81
ctgcagcccc ttctgttttt cttttgacgg                                   30


<210> 82
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer OAP3 for production of an expression
      cassette with AOX1 gene promoter and terminator

<400> 82
cccccggatc caggaacccg ggaacagaat ctagattttt tcgtaagtcg taagtcgtaa 60
cagaacacaa gagtctttga acaagttgag                                   90


<210> 83
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer OAT5 for production of an expression
      cassette with AOX1 gene promoter and terminator

<400> 83
cccccccgga tccgagacgg tgcccgactc ttgttcaatt cttttgg               47


<210> 84
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer OAT3 for production of an expression
      cassette with AOX1 gene promoter and terminator

<400> 84
cccataatgg taccgttagt ggtacgggca gtc                               33
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```
<210> 85
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer HGP5 for amplification of a gene conferring
      resistance against hygromycin B

<400> 85
gtcgacatga aaaagcctga actcaccgc                              29


<210> 86
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer HGP3 for amplification of a gene conferring
      resistance against hygromycin B

<400> 86
actagtctat tcctttgccc tcggacg                                27


<210> 87
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer for amplification of 5'-region of
      fi-mannosidase gene

<400> 87
gggggggtcga catggtggtc ttcagcaaaa ccgctgccc                   39


<210> 88
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer for amplification of 5'-region of
      fi-mannosidase gene

<400> 88
gggggggcggc cgcgtgatgt tgaggttgtt gtacggaacc ccc              43
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<210> 89
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer for amplification of Saccharomyces
      cerevisiae SUC2 gene

<400> 89
ggggactagt atgcttttgc aagctttcct tttccttttg   40

<210> 90
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer for amplification of Saccharomyces
      cerevisiae SUC2 gene

<400> 90
ccccagatct tattttactt cccttacttg gaacttgtc   39

<210> 91
<211> 711
<212> DNA
<213> Homo sapiens

<400> 91
ctcaccatga gggtccccgc tcagctcctg gggctcctgc tgctctggct cccaggtgca 60
cgatgtgaca tccagatgac ccagtctcca tcttccgtgt ctgcatctgt aggagacaga 120
gtcaccatca cttgtcgggc gagtcaggtt attagcagct ggttagcctg gtatcagcag 180
aaaccaggga aagcccctaa gctcctgatc tatgctgcat ccagtttgca aagtggggtc 240
ccatcaaggt tcagcggcag tggatctggg acagatttca ctctcaccat cagcagcctg 300
cagcctgaag attttgcaac ttactattgt caacaggcta acagtttccc tccgacgttc 360
ggccaaggga ccaaggtgga aatcaaacgt acggtggctg caccatctgt cttcatcttc 420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgttg a   711

<210> 92
<211> 234
<212> PRT
<213> Homo sapiens

<400> 92
Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp Leu Pro
 1   5   10   15

Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser
            20   25   30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Val
        35   40   45

Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    50   55   60

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
65   70   75   80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
            85   90   95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn
            100   105   110

Ser Phe Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
    115   120   125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130   135   140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145   150   155   160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
            165   170   175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180   185   190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
    195   200   205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210   215   220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225   230

<210> 93
<211> 1428
<212> DNA
<213> Homo sapiens

<400> 93
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tgtgcagcct ctggattcac cttcagtagc tatagcatga ctgggtccg ccaggctcca 180
gggaaggggc tggagtgggt ctcatccatt agtagtagta gtagttacat atactacgca 240
gactcagtga agggccgatt caccatctcc agagacaacg ccaagaactc actgtatctg 300
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agatcggatt 360
attatggttc ggggagtcta ctactactac ggtatggacg tctggggcca agggaccacg 420
gtcaccgtct cctcagctag caccaagggc ccatcggtct tccccctggc accctcctcc 480
aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 540

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ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 600
gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 660
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 720
aagaaagttg agcccaaatc ttgtgacaaa actcacacat gcccaccgtg cccagcacct 780
gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg 840
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 900
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 960
gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1020
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accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1320
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1380
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatga             1428
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<210> 94
<211> 475
<212> PRT
<213> Homo sapiens

<400> 94
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Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
 1               5                  10                  15

Val Gln Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35          .           40                  45

Ser Ser Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Val Ser Ser Ile Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala
 65                 70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                85                  90                  95

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Asp Arg Ile Ile Met Val Arg Gly Val Tyr Tyr
            115                 120                 125

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
            130                 135                 140

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
145                 150                 155                 160

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
                165                 170                 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
            180                 185                 190
```

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
        195   200   205

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
    210   215   220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
225   230   235   240

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
            245   250   255

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
            260   265   270

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    275   280   285

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    290   295   300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305   310   315   320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            325   330   335

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
            340   345   350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    355   360   365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
    370   375   380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385   390   395   400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            405   410   415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        420   425   430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        435   440   445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    450   455   460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465   470   475

<210> 95
<211> 7
<212> PRT
<213> Saccharomyces cerevisiae

<400> 95
Val Gly Phe Leu Asp His Met
  1   5

<210> 96
<211> 7
<212> PRT
<213> Saccharomyces cerevisiae

<400> 96
Pro Ser Thr Lys Gly Val Leu
  1   5

<210> 97
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PHI5 for amplification of Ogataea minuta
      HIS3 gene

<220>
<221> modified_base
<222> (2)
<223> a, c, g or t

<220>
<221> modified_base
<222> (5)
<223> a, c, g or t

<220>
<221> modified_base
<222> (11)
<223> a, c, g or t

<400> 97
tnggnttyyt ngaycayatg   20

<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PHI3 for amplification of Ogataea minuta
      HIS3 gene

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<220>
<221> modified_base
<222> (3)
<223> a, c, g or t

<220>
<221> modified_base
<222> (6)
<223> a, c, g or t

<220>
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<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (15)
<223> a, c, g or t

<220>
<221> modified_base
<222> (18)
<223> a, c, g or t

<400> 98
arnacnccyt tngtnswngg                                    20


<210> 99
<211> 3831
<212> DNA
<213> Ogataea minuta

<400> 99
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ccagtgaaga tatccgggac ggttggaaca gctcttttat caacaagaaa tctgagattg 180
aggaaccagc gtccaacaca aaaagcgact ctgcttcgtc tgtcaagaag accaaggcga 240
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aattgggcga gctggaactg ttggaagaga ccgaacgatt cgcccagatc tcgtctcaag 360
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aggacgcgtt gatgatgaag tgttttgact acgagctgga cggtgactcc cagcgtgcca 480
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atcacattgt ttccagatgc gagattatca agcaagaaca cgaacaagag ggccaagaag 720
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cggtggaaga cgccgagggt gttttggaac tgtttgaccg ctgcggggtg attcagatac 960
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gcacttaatc catatttttg agaggaggca ttctaagaat ctctctagtt ttgttctcgc 1200
tcattgcttg cagttttttg agaatctcag agttcttcca cttctcaggc agcggggtga 1260
cgtcgtactt cttagtggcc caatagtaga tatcccagtc cggctcatca agcaatttgt 1320
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cgtactcttc cagttggtcc gcagtcatcg aagccaagta cttgtccgca aatctactca 1380
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ttgtttccac gtcctcattg tctcttggga ttggctcgac cctgatcttc agctctccgt 1500
cctcctcagt taacatggtg tgggtgtttg ctccctggcc aagtctggcc accgaggttg 1560
cgaatcttct tctggtcaca aatcctgtca gcttaagcat tttgtccgtt gtgagaccaa 1620
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ggaaagcagc gacagatcgg ccgaccgcga ctatcgacgc gacgataggg attttttttt 1740
ttaaaaaaaa gagtcaaaaa aacatcctga agagaaactt ttcatgggga accatgtcca 1800
ggagtcatcc gacggtatcc ctttacagtc aaaaaaacat gtctgaagag aacaagaaac 1860
gcaagctgga aaacggcaca aatgatgcaa aagctgctcg gtttgcagag gtgagaagag 1920
tcaccaatga aaccagcatc cagatcatcc tgaacttgga tggtggactc atcgagtgca 1980
aagagtcgat tcttggggcc acttacgaaa aagagagcca cgcggcacaa aatacgagtg 2040
cacaggtgat ctccatcaag acaggactcg gtttccttga ccacatgctg cacgcccttg 2100
ccaaacactc tggttggtca ttgattgtcg agtgtattgg ggacctgcac attgacgacc 2160
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gcgcgcacat cacgatgcac gtcgattgtc ttcgcgggtt caatgaccac caccgcagtg 2460
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atgatgttcc aagtacgaag ggagttttga tgtaactcca cacccaggag cttctactaa 2580
tattcagccc tctccctctt catcgtgtac agtttaacca tactagacta accaactccg 2640
ccgtattctc acgtagccgc aaccgaaagc cctggaaagc agatagtcta accaatcgag 2700
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<211> 238
<212> PRT
<213> Ogataea minuta

<400> 100

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            20                  25                  30

Ser Ile Gln Ile Ile Leu Asn Leu Asp Gly Gly Leu Ile Glu Cys Lys
       35                  40                  45
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Glu Ser Ile Leu Gly Ala Thr Tyr Glu Lys Glu Ser His Ala Ala Gln
    50              55              60

Asn Thr Ser Ala Gln Val Ile Ser Ile Lys Thr Gly Leu Gly Phe Leu
 65              70              75              80

Asp His Met Leu His Ala Leu Ala Lys His Ser Gly Trp Ser Leu Ile
                85              90              95

Val Glu Cys Ile Gly Asp Leu His Ile Asp Asp His His Thr Ala Glu
            100             105             110

Asp Val Gly Ile Ala Leu Gly Glu Thr Phe Lys Arg Ala Leu Gly Pro
            115             120             125

Val Lys Gly Leu Lys Arg Phe Gly His Ala Tyr Ala Pro Leu Asp Glu
    130             135             140

Ala Leu Ser Arg Ala Val Val Asp Leu Ser Asn Arg Pro Phe Ala Val
145             150             155             160

Val Glu Leu Gly Leu Arg Arg Glu Lys Ile Gly Asp Leu Ser Cys Glu
            165             170             175

Met Ile Pro His Val Leu Glu Ser Phe Ala Thr Ser Ala His Ile Thr
            180             185             190

Met His Val Asp Cys Leu Arg Gly Phe Asn Asp His His Arg Ser Glu
    195             200             205

Ser Ala Phe Lys Ala Leu Ala Val Ala Ile Arg Asp Ala Thr Ser Tyr
    210             215             220

Thr Gly Arg Asp Asp Val Pro Ser Thr Lys Gly Val Leu Met
225             230             235
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<210> 101
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DHI5

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<210> 102
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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      primer DHI3

<400> 102
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<210> 103
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<212> PRT
<213> Saccharomyces cerevisiae

<400> 103
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<210> 104
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<212> PRT
<213> Saccharomyces cerevisiae

<400> 104
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<210> 105
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PLE5 for amplification of Ogataea minuta
      LEU2 gene

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<223> a, c, g or t

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<223> a, c, g or t

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<223> a, c, g or t

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<222> (15)
<223> a, c, g or t

<400> 105
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<210> 106
<211> 21
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PLE3 for amplification of Ogataea minuta
      LEU2 gene

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<223> a, c, g or t

<400> 106
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<210> 107
<211> 5615
<212> DNA
<213> Ogataea minuta

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<210> 108
<211> 363
<212> PRT
<213> Ogataea minuta

<400> 108

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            20                  25                  30

Lys Pro Glu Ile Lys Phe Asn Phe Glu His His Leu Ile Gly Gly Ala
        35                  40                  45

Ala Ile Asp Ala Thr Gly Gln Pro Ile Thr Asp Ala Ala Leu Glu Ala
    50                  55                  60

Ser Lys Lys Ala Asp Ala Val Leu Leu Gly Ser Val Gly Gly Pro Lys
65                  70                  75                  80

Trp Gly Thr Gly Gln Val Arg Pro Glu Gln Gly Leu Leu Lys Ile Arg
                85                  90                  95

Lys Glu Leu Asn Leu Tyr Ala Asn Leu Arg Pro Cys Ser Phe Ala Ser
            100                 105                 110

Asp Ala Leu Leu Asp Leu Ser Pro Leu Lys Pro Glu Ile Val Arg Gly
            115                 120                 125
```

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Thr Asp Phe Val Val Val Arg Glu Leu Val Gly Gly Ile Tyr Phe Gly
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Glu Arg Lys Glu Asp Asp Gly Ser Gly Phe Ala Ser Asp Thr Glu Ala
145             150             155             160

Tyr Ser Val Pro Glu Val Gln Arg Ile Thr Arg Met Ala Ala Phe Met
                165             170             175

Ala Leu Gln Ser Asp Pro Pro Leu Pro Val Tyr Ser Leu Asp Lys Ala
            180             185             190

Asn Val Leu Ala Ser Ser Arg Leu Trp Arg Lys Thr Val Glu Glu Thr
        195              200             205

Ile Lys Asn Glu Phe Pro Gln Leu Lys Leu Gln His His Leu Ile Asp
    210             215             220

Ser Ala Ala Met Ile Leu Val Lys Ser Pro Thr Lys Leu Asn Gly Val
225             230             235             240

Val Leu Thr Ser Asn Met Phe Gly Asp Ile Ile Ser Asp Glu Ala Ser
            245             250             255

Val Ile Pro Gly Ser Leu Gly Leu Leu Pro Ser Ala Ser Leu Ala Ser
            260             265             270

Leu Pro Asp Ser Asn Glu Ala Phe Gly Leu Tyr Glu Pro Cys His Gly
        275             280             285

Ser Ala Pro Asp Leu Ala Lys Gly Leu Val Asn Pro Leu Ala Thr Ile
    290             295             300

Leu Ser Ala Ala Met Met Leu Lys Leu Ser Leu Asn Leu Val Glu Glu
305             310             315             320

Gly Arg Ala Val Glu Lys Ala Val Arg Ala Val Leu Asp Gln Gly Ile
            325             330             335

Met Thr Ala Asp Leu Gly Gly Ser Ser Ser Thr Thr Glu Val Gly Asp
            340             345             350

Ala Val Ala Lys Glu Val Thr Lys Leu Leu Gly
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<210> 109
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DL5

<400> 109
caggagctac agagtcatcg                                              20
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<210> 110
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DL3

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<210> 111
<211> 8
<212> PRT
<213> Saccharomyces cerevisiae

<400> 111
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<210> 112
<211> 8
<212> PRT
<213> Saccharomyces cerevisiae

<400> 112
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  1   5

<210> 113
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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      primer PLE5 for amplification of Ogataea minuta YPS1 gene

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<220>
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<220>
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<400> 113
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<210> 114
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      primer PLE3 for amplification of Ogataea minuta YPS1 gene

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<210> 115
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<212> DNA
<213> Ogataea minuta

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Glu Ile Tyr Arg Gly His Ser Phe Glu Thr Ser Gln Arg Gly Gly Arg
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Pro Tyr Met Leu Glu Lys Arg Ala Glu Asp Gly Ser Val Leu Met Glu
    50   55   60

Leu Gln Asn Asn Gln Ser Phe Tyr Lys Val Glu Leu Glu Val Gly Ser
65   70   75   80

Asp Lys Gln Lys Ile Gly Val Leu Val Asp Thr Gly Ser Ser Asp Leu
                85   90   95

Trp Ile Met Asn Gln Asn Asn Ser Tyr Cys Glu Ser Ser Ser Ser Ser
            100   105   110

Ser Lys Met Arg Glu Arg Lys Gly Arg Lys Leu Ser Asp Leu Arg Asn
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Leu Asn Leu Asp Val Ser Glu Lys Asn Val Lys Ala Val Gly Ala Ala
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Glu Thr Glu Thr Met Thr Leu Ser Val Gly Glu Gly Leu Phe Ser Trp
145   150   155   160

Phe Glu Thr Gln Thr Asp Gly Ser Gly Glu Thr Glu Thr Ala Ser
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Gly Asp Ser Ser Glu Ala Thr Ile Asp Cys Ser Val Tyr Gly Thr Phe
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Asp Pro Ser Ser Ser Asp Thr Phe Lys Ser Asn Gly Thr Glu Phe Ser
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Ile Ser Tyr Ala Asp Asp Ser Phe Ala Lys Gly Thr Trp Gly Thr Asp
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Asp Val Thr Phe Asn Gly Val Thr Val Asp Gln Leu Ser Met Ala Ile
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Ala Asp Glu Thr Asn Ser Ser Met Gly Val Leu Gly Ile Gly Leu Lys
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Glu Asn Leu Pro Tyr Lys Met Gln Ser Gln Gly Leu Ile Ser Lys Pro
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Val Tyr Ser Val Tyr Leu Asn Asp Ser Glu Ser Ser Ala Ala Ser Ile
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Leu Phe Gly Ala Val Asp His Asp Lys Tyr Thr Gly Thr Leu Thr Leu
305   310   315   320

Leu Pro Ile Ile Asn Thr Ala Glu Ser Leu Gly Tyr Ser Thr Pro Val
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Arg Leu Glu Val Thr Leu Ser Lys Leu Tyr Thr Gly Ser Ser Ser Asn
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Lys Thr Ala Val Ser Ile Ala Ser Gly Ala Ala Ala Ala Leu Leu Asp
         355   360   365

Thr Gly Thr Thr Leu Thr Tyr Val Pro Ser Asp Ile Ile Ser Thr Ile
    370   375   380

Val Asp Gln Tyr Gly Phe Gln Tyr Ser Ser Ser Val Gly Thr Tyr Val
385   390   395   400

Ala Lys Cys Asp Ser Leu Asp Asp Ala Glu Ile Val Phe Asp Phe Gln
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Gly Thr Lys Ile Trp Val Pro Phe Ser Ser Phe Ala Val Ser Leu Thr
         420   425   430

Thr Asn Gly Gly Ser Gln Ser Ser Tyr Cys Ala Leu Gly Leu Met Asp
         435   440   445

Ser Gly Asp Asp Thr Phe Thr Leu Gly Asp Ser Phe Leu Asn Asn Val
    450   455   460

Tyr Phe Val Ala Asp Leu Glu Asn Leu Gln Ile Ala Ile Ala Pro Ala
465   470   475   480

Asn Leu Asp Ser Thr Ser Glu Asp Ile Glu Val Val Ser Asp Ser Gly
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Ile Pro Ser Ala Lys Ser Ala Ser Ala Tyr Ser Ser Ser Trp Gly Ala
         500   505   510

Ser Gly Ser Ala Val Ala Ser Ser Leu Ser Val Gln Thr Gly Ala Glu
         515   520   525

Thr Val Thr Ser Thr Asp Ala Gly Ser Asp Ser Thr Gly Ser Ala Ser
    530   535   540

Gly Ser Ser Gly Ser Ala Ser Ser Ser Ser Ser Lys Ser Ser Ala Ser
545   550   555   560

Ser Ser Ser Gly Ser Ser Gly Ser Ser Ser Lys Ser Gly Ser Ser Ser
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Ser Lys Tyr Ala Ala Gly Asn Ala Trp Gly Met Ser Val Cys Ser Leu
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